

PATENT
USSN 08/974,584
015389-002950US
018/206p2

APPENDIX B**BEST AVAILABLE COPY****Human TERT protein sequence**

LOCUS 014746 1132 aa linear PRI 15-JUN-2002
DEFINITION Telomerase reverse transcriptase (Telomerase catalytic subunit)
ORGANISM Homo sapiens
AUTHORS Nakamura,T.M., Morin,G.B., Chapman,K.B., Weinrich,S.L.,
Andrews,W.H., Lingner,J., Harley,C.B. and Cech,T.R.
TITLE Telomerase catalytic subunit homologs from fission yeast and human
JOURNAL Science 277 (5328), 955-959 (1997)

```
1 mprapr crav rsllrshyre vlplatfvrr lgpqgwrlvq rgdpaafraI vaqclvcvpw
61 darpppaaps frqvscikel varvlqrIce rgaknvlaIq falldgargg ppeafttsvr
121 sylpntvt da lrgsgawgll lrrvgddvlv hllarcalfv lvapscayqv cgppllyqlga
181 atqarpppha sgprrrlgce rawnhsvrea gvpIglpapg arrrggsasr slplpkrprrr
241 gaapepertp vggqswahpg rtrgpsdrgr cvvsparpae eatslegals gtrhshpsvg
301 rqhha gppst srpprpwdtp cppvyaetkh flyssgdkeq lrpsfllssl rpsltgarrl
361 vetiflgsrp wmpgtprrlp rlpqrywqmr plfllellgnh aqcpygvllk thcplraavt
421 paagvcarek pqgsvaapee edtdprrlvq llrqhsspwq vygfvracIr rlvppglwgs
481 rhnerrflrn tkkfislghk aklsIqeltw kmsvrdcawl rrspgvgcvp aaehrIreei
541 lakflhwImS vyvvellrsf fyvtettfqq nrllfyrksv wsklqsIgr qhlkrvqlre
601 lseaevrqhr earpalltsr lrfipkpdgl rpivnm dyvv gartfrrekr aerltsrvka
661 lfsvl nyera rrp gllgasv lglddihrav rtfvlrvraq dpppelyfvk vdvtagaydti
721 p qdr ltevia sllkpqntyc vrryavvqka ahghvrkafk shvstltdlq pymrqfvahl
781 qetsplrdav vieqssslne assglfdvfl rfmchhavri rgksyvqcqg ipqgsilstl
841 lcsIcygdme nkIfaglrnd gllrlrvddf llvtphltha ktflrtlvrg vpeygcvvnl
901 rktvvnfpve dealggtafv qmpahglfpw cgllldtrtl evqsdysyya rtsirasltf
961 nrgfkagrnM rrrklfgvlrl kchslfidlq vnsIqtvcctn Iykilllqay rfhacvlqlp
1021 fhqqvwknpt fflrvisdta slcysllkak nagmslgakg aagplpseav qwlchqafll
1081 kltrhrvtvY pllgslrtaq tqIsrkIpgt tltaIeaaan palpsdfkti ld
```

BEST AVAILABLE COPY



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

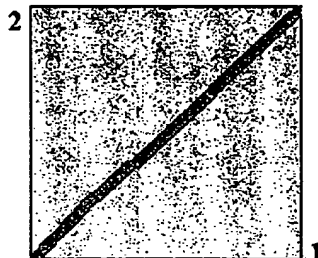
Matrix **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ View option **Standard**Masking character option **X for protein, n for nucleotide** Masking color option **Black**☐ Show CDS translation

Sequence 1: lcl|seq_1

Length = 1132 (1 .. 1132)

Sequence 2: lcl|seq_2

Length = 1122 (1 .. 1122)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1340 bits (3468), Expect = 0.0

Identities = 715/1146 (62%), Positives = 839/1146 (73%), Gaps = 38/1146 (3%)

Query	1	MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPQGWRLLVQRGDPAAFRALVAQCLVCVPW	60
		M RAPRC AVRSLRS YREV PLATFVRRLLGP+G RLVQ GDP +R LVAQCLVC+ W	
Sbjct	1	MTRAPRCFAVRSLLRSRYREVWPLATFVRRLLGPEGRRLLVQPGDPKIYRTLVAQCLVCMHW	60
Query	61	DARPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR	120
		++PPPA SF QVS LKELVARV+QRLCER +NVLAFGF LL+ ARGGPP AFT+SVR	
Sbjct	61	GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120
Query	121	SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180
		SYLPNTV + LR SGAW LLL RVGDD+LV+LLA CAL++LV PSCAYQVCG PLYQ+ A	
Sbjct	121	SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA	180
Query	181	ATQARPPPHAS-GPRRRLG-----CERAWNHSVREAGVPLGLPAPGARRRGGSASRS	231
		T P AS P R +G ++ + S +EA PL LP+ G +R S S	
Sbjct	181	TTDIWPSVSASYPTRPVRNFTNLRFLQIQSSSRQEAPKPLALPSRGTKRHLSTSTS	240

Query	232	LPLPKRPRRGAAPEPERTFVGQGSWAHPGRTRGPSDRGFCVVSARP-AEEATSLEGALS	290
		+P K+ R P E P Q G++ PS SP P AE+ S +G +S	
Sbjct	241	VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVSPAR----SPEVPTAEKDLSSKGKVS	296
Query	291	GTRHSHPSVGRQHAGPPSTSRPPRPWDTPCPPVYAETHFLYSSGD-KEQLRPSFLLSS	349
		S SV +H S PPR P + ET+HFLYS GD +E+L PSFLLS+	
Sbjct	297	DLSLSG-SVCKCHKPSSTSLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSFLLSN	354
Query	350	LRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPGVLL	409
		L+P+LTGARRLVE IFLGSRP G R RL +RYWQMRPLF +LL NHA+C Y LL	
Sbjct	355	LQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLL	414
Query	410	KTHCPLRAAVTPAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACL	469
		++HC R A + + +T P L+ LLR HSSPWQVYGF+RACL	
Sbjct	415	RSHCRFRTA-----NQQVTDALNTSPPHLMDLLRLHSSPWQVYGF+RACL	459
Query	470	RRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCV	529
		++V LWG+RHNERRF +N KKFISLGK+ KLSLQEL WKM V DC WLR SPG V	
Sbjct	460	CKVVSASLWGRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRSPPGKDRV	519
Query	530	PAAEHLREEILAKFLHWMVSVYVVELLSFFYVTETTFQKNRFFYRKSVWSKLQSIGI	589
		PAAEHLRE ILA FL WLM YVV+LLRSFFY+TE+TFQKNRFFYRKSVWSKLQSIG+	
Sbjct	520	PAAEHLRERILATFLFWLMDTYVVQLLSFFYITESTFQKNRFFYRKSVWSKLQSIGV	579
Query	590	RQHLKRVQLRELSAEVRQHREARPALLSRLRFIPKPDGLRPIVNM DYVVGARTFRREK	649
		RQHL+RV+LRELS+ EVR H++ A+ RLRFPKP+GLRPIVNM Y +G R R K	
Sbjct	580	RQHLEVRVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNM SYSMTALGRRK	639
Query	650	RAERLTSRVKALFVSVLNYERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFV	709
		+A+ T R+K LFS+LNYER + P L+G+SVLG++DI+R WR FVLRVRA D P +YFV	
Sbjct	640	QAQHFTQRLKTLFMSLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFV	699
Query	710	KVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTD	768
		K DVTGAYD IPQ +L EV+A++I+ ++TYC+R+YAVV++ + G V K+F+ V+TL+D	
Sbjct	700	KADVTGAYDAIPQGLVEVVANMIRHSESTYCIQYAVVRRDSQQQVHKSFRRQVTTLS	759
Query	769	LQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYV	826
		LQPYM QF+ HLQ++ S LR++VVIEQS S+NE+SS LFD FL F+ H V+I + Y	
Sbjct	760	LQPYMGQFLKHLQSDASALRNSVVIEQSSISMNESSSLFDFFLHFLRHSVVKIGDRCYT	819
Query	827	QCQGIPOGSILSTLLCSLCYGD MENKLFAGIRRDGLLLRLVODFLLVTPHLTHAKTFLRT	886
		QCQGIPOGS LSTLLCSLC+GD MENKLF A ++RDGLLLR VDDFLLVTPHL AKTFL T	
Sbjct	820	QCQGIPOGSSLSTLLCSLCFGD MENKLF AEVQRDGLLLRFVDDFLLVTPHL DQAKTFLST	879
Query	887	LVRGVPEYGCVVNLRKTVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDY	946
		LV GVPEYGC++NL+KTVNFPVE LGG A Q+PAH LFPWCGLLLD+TLEV DY	
Sbjct	880	LVHGVPEYGC MINLQKTVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDQTLEVFCDY	939
Query	947	SSYARTSIRASLTFNRGFKAGRNMRRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILL	1006
		S YA+TSI+ SLTF FKAG+ MR KL VLRLKCH LFLDLQVNSLQTVCTNIYKI L	
Sbjct	940	SGYAQTSIKTSLTFQSVFKAGTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCTINIYKIFL	999
Query	1007	LQAYRFHACVLQLPFHQQVWKNPTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAAGPLP	1066
		LQAYRFHACV+QLPF Q+V KN TFFL +IS AS CY+ILK KN GM+L A G+ P	
Sbjct	1000	LQAYRFHACVQLPFDQVRKNLTFFLGISSQASCCYAILKVKNPGMTLKASGS---FP	1056
Query	1067	SEAVQWLCHQAFLKLTRHRVTVYVPLLSLRTAQTLRSRKLPGTTLTALEAAANPALPSD	1126
		EA WLC+QAFLLKL H V Y LLG LRTAQ L RKLP T+T L+AAA+PAL +D	
Sbjct	1057	PEAAHWLCYQAFLKLAAHSVYIKCLLGLPLRTAQKLLCRKLPEATMTILKAAADPALSTD	1116

Query 1127 FKTILD 1132
F+TILD
Sbjct 1117 FQTILD 1122

CPU time: 0.07 user secs. 0.00 sys. secs 0.07 total secs.

Lambda K H
0.324 0.138 0.434

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 9278

Number of extensions: 5864

Number of successful extensions: 8

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 1132

Length of database: 1,129,354,045

Length adjustment: 144

Effective length of query: 988

Effective length of database: 1,129,353,901

Effective search space: 1115801654188

Effective search space used: 1115801654188

Neighboring words threshold: 9

X1: 15 (7.0 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 40 (21.6 bits)

S2: 84 (37.0 bits)